

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: April 12, 2004, 10:18:37 ; Search time 21 seconds  
(without alignments)  
1543.645 Million cell updates/sec

Title: US-10-025-730-1

Perfect score: 1704

Sequence: 1 MKQPLFSKSHKNPAEIVKI.....FADENKYLKQIRIDIKTAP 337

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1376	80.8	341	2	157997
2	1063.5	62.4	377	2	116651
3	1006.5	59.1	338	2	127129
4	834.5	49.0	329	2	150117
5	685	40.2	305	2	671441
6	632	37.1	348	2	884448
7	485	28.5	399	2	834681
8	143.5	8.4	339	2	133477
9	134.5	7.9	677	2	164574
10	128	7.5	430	2	164709
11	125.5	7.4	298	2	164854
12	125.5	7.4	1642	2	108880
13	123.5	7.2	1285	2	872420
14	120	7.0	1175	2	164469
15	118.5	7.0	959	2	100246
16	115	6.7	474	2	171322
17	113.5	6.7	833	2	143446
18	112.5	6.6	1411	2	155133
19	111.5	6.5	725	1	105016
20	111.5	6.5	2401	2	128676
21	111	6.5	2166	2	670153
22	111	6.5	2819	2	890551
23	109.5	6.4	457	2	882911
24	109.5	6.4	978	2	147087
25	109.5	6.4	1830	2	182909
26	109	6.4	695	2	107283
27	109	6.4	1401	2	151527
28	108.5	6.4	442	2	118507
29	108.5	6.4	952	2	150451

30	108.5	6.4	1163	2	D64315	type I restriction
31	108	6.3	568	2	873254	replication helica
32	107.5	6.3	483	2	140055	positive trans-act
33	107.5	6.3	855	2	E90106	importin beta-1 su
34	107.5	6.3	1042	2	G64514	type I restriction
35	107.5	6.3	1726	1	SAZQCM	major mercozole su
36	107.5	6.3	1726	2	A45948	major mercozole su
37	107	6.3	570	2	S68686	phosphoprotein pho
38	107	6.3	1173	2	T43527	sp8 protein - figs
39	107	6.3	1727	2	150073	myosin-like coiled
40	106	6.2	474	2	S56748	glutathione syntha
41	106	6.2	1295	2	T24587	hypothetical prote
42	105.5	6.2	781	2	T00456	protein kinase hom
43	105.5	6.2	847	2	A56039	GTPase-activating
44	105.5	6.2	1091	2	T34107	hypothetical prote
45	105.5	6.2	1619	2	T18499	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

157997  
hypothetical calcium-binding protein - mouse

C/Species: Mus sp. (mouse)  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #ext\_change 19-May-2000

C/Accession: 157997

R/Miyamoto, H.; Matsushiro, A.; Nozaki, M.

Mol. Reprod. Dev. 34, 1-7, 1993

A/Title: Molecular cloning of a novel mRNA sequence expressed in cleavage stage mou

A/Reference number: 157997; MUID:3119656; PMID:8418609

A/Accession: 157997

A/Status: preliminary; translated from GB/EHBL/DD81

A/Molecule type: mRNA

A/Residues: 1-341 <RES>

A/Cross-References: GB:S51858; NID:9262933; PIDN:AAB24801.1; PID:9262934

C/Superfamily: Saccharomyces hypothetical protein YKU189w

C/Keywords: calcium binding

Query Match 80.8%; Score 1376; DB 2; Length 341;

Best Local Similarity 80.7%; Pred. No. 7.9e-85;

Matches 272; Conservative 32; Mismatches 29; Indels 4; Gaps 2;

QY	4	MPF-PSKSHKNPAEIVKILKDNALIEKQ--DKTDKASEVSKSLQMKSLGCTNEK	59
DB	1	MPFPGKSHKSPADIVKILKESMAVLEKODISPKAKAKTEBVSXKLVAMKILVGTNEK	60
QY	60	EPPTAAVAKQIAOEYSSGLVTLADQLDFEGKXDYVQIFNNILRQIGRSPVETI	119
DB	61	EPQTAVAQIAOEYNSGLVTLADQLDFEGKDVAVQIFNNILRQIGRTPVETI	120
QY	120	SNAPRILFMILKGYEADQIALRCGIMLRBCIRHPEPLAKIILFENQFRDFKVELSTEDI	179
DB	121	CQOQIILFMILKGYEADQIALRCGIMLRBCIRHPEPLAKIILFENQFRDFKVELSTEDI	180
QY	180	ASDAATRKDILTRKVLVADFLQNDPIFEDYEKLQSENVVTRQSLKLGELIDR	239
DB	181	ASDAATRKDILTRKVLVADFLQNDPIFEDYEKLQSENVVTRQSLKLGELIDR	240
QY	240	HNFAIMTKYISKPENLKLMMNLADKSPNIOFAEFVFKVFAVSPKPTPIVEILKNOP	299
DB	241	HNFTIMTKYISKPENLKLMMNLADKSPNIOFAEFVFKVFAVSPKPTPIVEILKNOP	300
QY	300	KLIETLSFQKERRDDQFADENKYLKQIRIDIKTAP 336	
DB	301	KLIETLSFQKERRDDQFADENKYLKQIRIDIKTAP 337	

##### RESULT 2

11651  
hypothetical protein R02E12.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #ext\_change 18-Feb-2000